

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,883

DATE: 06/05/2001

TIME: 08:27:24

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I854883.raw

P.5
ENTERED

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4 <110> APPLICANT: Lex M. Cowsert
5 Jacqueline Wyatt
6 Susan M. Freier
7 Brett P. Monia
8 Madeline M. Butler
9 Robert McKay
11 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
13 <130> FILE REFERENCE: ISPH-0576
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/854,883
C--> 15 <141> CURRENT FILING DATE: 2001-05-14
15 <150> PRIOR APPLICATION NUMBER: US 09/629,644
16 <151> PRIOR FILING DATE: 2000-07-31
18 <150> PRIOR APPLICATION NUMBER: US 09/487,368
19 <151> PRIOR FILING DATE: 2000-01-18
21 <160> NUMBER OF SEQ ID NOS: 389
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 20
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
31 <223> OTHER INFORMATION: Antisense Oligonucleotide
33 <400> SEQUENCE: 1
34 tccgtcatcg ctctcaggg 20
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 20
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
45 <223> OTHER INFORMATION: Antisense Oligonucleotide
47 <400> SEQUENCE: 2
48 atgcattctg cccccaagga 20
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 3247
52 <212> TYPE: DNA
53 <213> ORGANISM: Homo sapiens
55 <220> FEATURE:
56 <221> NAME/KEY: CDS
57 <222> LOCATION: (91)...(1398)
59 <400> SEQUENCE: 3
60 gggcgggcct cggggctaag agcgcgacgc ctagagcggc agacggcgca gtgggccgag 60
62 aaggaggcgc agcagccgcc ctggcccgtc atg gag atg gaa aag gag ttc gag 114
63 Met Glu Met Glu Lys Glu Phe Glu
64 1 5
66 cag atc gac aag tcc ggg agc tgg gcg gcc att tac cag gat atc cga 162
67 Gln Ile Asp Lys Ser Gly Ser Trp Ala Ala Ile Tyr Gln Asp Ile Arg
68 10 15 20
69 cat gaa gcc agt gac ttc cca tgt aga gtg gcc aag ctt cct aag aac 210

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70 His Glu Ala Ser Asp Phe Pro Cys Arg Val Ala Lys Leu Pro Lys Asn
71 25 30 35 40
73 aaa aac cga aat agg tac aga gac gtc agt ccc ttt gac cat agt cgg 258
74 Lys Asn Arg Asn Arg Tyr Arg Asp Val Ser Pro Phe Asp His Ser Arg
75 45 50 55
77 att aaa cta cat caa gaa gat aat gac tat atc aac gct agt ttg ata 306
78 Ile Lys Leu His Gln Glu Asp Asn Asp Tyr Ile Asn Ala Ser Leu Ile
79 60 65 70
81 aaa atg gaa gaa gcc caa agg agt tac att ctt acc cag gcc cct ttg 354
82 Lys Met Glu Glu Ala Gln Arg Ser Tyr Ile Leu Thr Gln Gly Pro Leu
83 75 80 85
85 cct aac aca tgc ggt cac ttt tgg gag atg gtg tgg gag cag aaa agc 402
86 Pro Asn Thr Cys Gly His Phe Trp Glu Met Val Trp Glu Gln Lys Ser
87 90 95 100
89 agg ggt gtc gtc atg ctc aac aga gtg atg gag aaa ggt tgc tta aaa 450
90 Arg Gly Val Val Met Leu Asn Arg Val Met Glu Lys Gly Ser Leu Lys
91 105 110 115
93 tgc gca caa tac tgg cca caa aaa gaa gaa aaa gag atg atc ttt gaa 498
94 Cys Ala Gln Tyr Trp Pro Gln Lys Glu Glu Lys Glu Met Ile Phe Glu
95 125 130 135
97 gac aca aat ttg aaa tta aca ttg atc tct gaa gat atc aag tca tat 546
98 Asp Thr Asn Leu Lys Leu Thr Leu Ile Ser Glu Asp Ile Lys Ser Tyr
99 140 145 150
101 tat aca gtg cga cag cta gaa ttg gaa aac ctt aca acc caa gaa act 594
102 Tyr Thr Val Arg Gln Leu Glu Leu Glu Asn Leu Thr Thr Gln Glu Thr
103 155 160 165
105 cga gag atc tta cat ttc cac tat acc aca tgg cct gac ttt gga gtc 642
106 Arg Glu Ile Leu His Phe His Tyr Thr Thr Trp Pro Asp Phe Gly Val
107 170 175 180
109 cct gaa tca cca gcc tca ttc ttg aac ttt ctt ttc aaa gtc cga gag 690
110 Pro Glu Ser Pro Ala Ser Phe Leu Asn Phe Leu Phe Lys Val Arg Glu
111 185 190 195
113 tca ggg tca ctc agc ccg gag cac ggg ccc gtt gtg gtg cac tgc agt 738
114 Ser Gly Ser Leu Ser Pro Glu His Gly Pro Val Val Val His Cys Ser
115 205 210 215
117 gca ggc atc ggc agg tct gga acc ttc tgt ctg gct gat acc tgc ctc 786
118 Ala Gly Ile Gly Arg Ser Gly Thr Phe Cys Leu Ala Asp Thr Cys Leu
119 220 225 230
121 ctg ctg atg gac aag agg aaa gac cct tct tcc gtt gat atc aag aaa 834
122 Leu Leu Met Asp Lys Arg Lys Asp Pro Ser Ser Val Asp Ile Lys Lys
123 235 240 245
125 gtg ctg tta gaa atg agg aag ttt cgg atg ggg ttg atc cag aca gcc 882
126 Val Leu Leu Glu Met Arg Lys Phe Arg Met Gly Leu Ile Gln Thr Ala
127 250 255 260
128 gac cag ctg cgc ttc tcc tac ctg gct gtg atc gaa ggt gcc aaa ttc 930
129 Asp Gln Leu Arg Phe Ser Tyr Leu Ala Val Ile Glu Gly Ala Lys Phe
130 265 270 275
132 atc atg ggg gac tct tcc gtg cag gat cag tgg aag gac ctt tcc cac 978
133 Ile Met Gly Asp Ser Ser Val Gln Asp Gln Trp Lys Glu Leu Ser His

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134                               285                               290                               295
136 gag gac ctg gag ccc cca ccc gag cat atc ccc cca cct ccc cgg cca      1026
137 Glu Asp Leu Glu Pro Pro Pro Glu His Ile-Pro Pro Pro Pro Arg Pro
138                               300                               305                               310
140 ccc aaa cga atc ctg gag cca cac aat ggg aaa tgc agg gag ttc ttc
141 Pro Lys Arg Ile Leu Glu Pro His Asn Gly Lys Cys Arg Glu Phe Phe      1074
142                               315                               320                               325
144 cca aat cac cag tgg gtg aag gaa gag acc cag gag gat aaa gac tgc
145 Pro Asn His Gln Trp Val Lys Glu Glu Thr Gln Glu Asp Lys Asp Cys      1122
146                               330                               335                               340
148 ccc atc aag gaa gaa aaa gga agc ccc tta aat gcc gca ccc tac ggc
149 Pro Ile Lys Glu Glu Lys Gly Ser Pro Leu Asn Ala Ala Pro Tyr Gly      1170
150                               345                               350                               355
152 atc gaa agc atg agt caa gac act gaa gtt aga agt cgg gtc gtg ggg
153 Ile Glu Ser Met Ser Gln Asp Thr Glu Val Arg Ser Arg Val Val Gly      1218
154                               365                               370                               375
156 gga agt ctt cga ggt gcc cag gct gcc tcc cca gcc aaa ggg gag cgg
157 Gly Ser Leu Arg Gly Ala Gln Ala Ala Ser Pro Ala Lys Gly Glu Pro      1266
158                               380                               385                               390
160 tca ctg ccc gag aag gac gag gac cat gca ctg agt tac tgg aag ccc
161 Ser Leu Pro Glu Lys Asp Glu Asp His Ala Leu Ser Tyr Trp Lys Pro      1314
162                               395                               400                               405
164 ttc ctg gtc aac atg tgc gtg gct acg gtc ctc acg gcc ggc gct tac
165 Phe Leu Val Asn Met Cys Val Ala Thr Val Leu Thr Ala Gly Ala Tyr      1362
166                               410                               415                               420
168 ctc tgc tac agg ttc ctg ttc aac agc aac aca tag cctgaccctc
169 Leu Cys Tyr Arg Phe Leu Phe Asn Ser Asn Thr      1408
170                               425                               430                               435
172 ctccactcca cctccaccaca ctgtccgct ctgcccgag agccccagcc cgactagcag      1468
174 gcactgccgg gtaggtaagg gcgcgcggac cgcgtagaga gccggggccc ggacgagcgt      1528
176 tggttctgca ctaaaaccaca tcttccccgg atgtgtgtct caccctcat ccttttactt      1588
178 ttgtccctct ccaacttgag taccaaatcc acaagccatt ttttgaggag agtgaagag      1648
180 agtaccatgc tggcgcgca gaggggaagg gctacacccc gtcttggggc tcgcccaccc      1708
182 cagggtccc tcttggaaga tcccaggcgg cgcacgcccac cagccccccc ctggaatctg      1768
184 cagggaqcaa ccttccactc catatttatt taacaattt tttcccaaaa ggcattcata      1828
186 gtgcaactag attttcttga accaataatg tattaataatt tttgtatgc agccttgcat      1888
188 caagggtctt atcaaaaagt acaataataa atctccaggt agtactggga atggaaggct      1948
189 ttgcctgggg cctgctgcgt cagaccagta ctgggaagga ggacggttgt aagcagttgt      2008
191 tatttagtga tattgtgggt aacgtgagaa gatagacaaa tgcataata tataatgaac      2068
193 acgtgggtat ttaataagaa acatgatgtg agattacttt gtcccgtta ttctctccc      2128
195 tgttatctgc tagatctagt tctcaatcac tgcctcccgc tgtgtattag aatgcattga      2188
197 aggtctctct gtgtctgat gaaaatatg tgcctggaat gagaaacttt gatctctgct      2248
199 tactaatgtg ccccatgtcc aagtcacaac tgcctgtgca tgacctgacg attacatggc      2308
201 tgtggttctt aagcctgttg ctgaagtcac tgtcgtcag caatagggtg cagttttcca      2368
203 ggaataggca ttgtctaatt cctggcatga cactctagt acttctggt gagggccagc      2428
205 cgtctcgtgt acagcagggt ctgtcgttaa ctcagacatt ccaagggtat gggaagccat      2488
207 attcacacct cagctctggg acatgattta gggaagcagg gacacccccc gcccccacct      2548
209 ttgtggatca cctctcccca ttccaagtca acactctct tgagcagacc gtgatttggg      2608
211 agagaggcac ctgctggaaa ccacactctc tgaacacgac tgggtgacgg tccttttaggc      2668

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213 agcctgcgcg cgtctctgtc ccggttcacc ttgccgagag aggcgcgtct gcccaccct 2728
215 caaacctctgt ggggcctgat ggtgctcacc actcttctgt caaagggaac tgaagacctc 2788
217 cacattaagt gcctttttta catgaaaaac acggcagctg tagctcccg gctactctct 2848
219 tgcacgacatt ttcacatttt gcctttctcg tggtagaagc cagtcacag aaattctgtg 2908
221 gtgggaacat tcgaggtgtc accctgcaga gctatggtga ggtgtggata aggcttagtg 2968
223 gccagggctgt aagcattctg agctggcttg ttgtttttaa gtctctgtata tgtatgtagt 3028
225 agtttgggtg tgtatatata gtatgcattc aaaatggacg tactgtttta acctctatc 3088
227 ctggagagac agctggctct ccaccttggt acacattatg tttagagaggt agcgagctgc 3148
229 tctgctatat gccttaagcc aatatttact catcaggtca ttatttttta caatggccat 3208
231 ggaataaacc atttttaca aaataaaaac aaaaaaagc 3247
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 21
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
242 <223> OTHER INFORMATION: PCR Primer
244 <400> SEQUENCE: 4
245 ggagttcgag cagatcgaca a
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 21
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 5
259 ggccactcta catgggaagt c
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 24
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
270 <223> OTHER INFORMATION: PCR Probe
272 <400> SEQUENCE: 6
273 agctggggcg ccatttacca ggat
276 <210> SEQ ID NO: 7
277 <211> LENGTH: 19
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
284 <223> OTHER INFORMATION: PCR Primer
286 <400> SEQUENCE: 7
287 gaaggtgaag gtcggagtc
290 <210> SEQ ID NO: 8
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
298 <223> OTHER INFORMATION: PCR Primer
300 <400> SEQUENCE: 8

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Output Set: C:\CRF3\06052001\I854883.raw

```

301 gaagatgggt atgggatttc
304 <210> SEQ ID NO: 9
305 <211> LENGTH: 20
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
312 <223> OTHER INFORMATION: PCR Probe
314 <400> SEQUENCE: 9
315 caagcttccc gttctcagcc
318 <210> SEQ ID NO: 10
319 <211> LENGTH: 4127
320 <212> TYPE: DNA
321 <213> ORGANISM: Rattus norvegicus
323 <220> FEATURE:
324 <221> NAME/KEY: CDS
325 <222> LOCATION: (120)...(1418)
327 <400> SEQUENCE: 10
328 agccgctgct ggggaggttg gggctgaggt ggtggcgggc gacgggcctc gagacgcgga 60
330 gcgacgcggc ctagcgcggc gacggccga ggggaactcg gcagtcgtcc cgtcccgcc 119
334 atg gaa atg gag aag gaa ttc gag cag atc gat aag gct ggg aac tgg 167
335 Met Glu Met Glu Lys Glu Phe Glu Gln Ile Asp Lys Ala Gly Asn Trp
336 1 5 10 15
338 gcg gct att tac cag gat att cga cat gaa gcc agt gac ttc cca tgc
339 Ala Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys 215
340 20 25 30
342 aga ata gcg aaa ctt cct aag aac aaa aac cgg aac agg tac cga gat
343 Arg Ile Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp 263
344 35 40 45
346 gtc agc cct ttt gac cac agt cgg att aaa ttg cat cag gaa gat aat
347 Val Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn 311
348 50 55 60
350 gac tat atc aat gcc agc ttg ata aaa atg gag gaa gcc cag agg agc
351 Asp Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser 359
352 65 70 75 80
354 tat atc ctc acc cag gcc cct tta cca aac acg tgc ggg cac ttc tgg
355 Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp 407
356 85 90 95
358 gag atg gtg tgg gag cag aag agc agg gcc gtg gtc atg etc aac cgc
359 Glu Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg 455
360 100 105 110
362 atc atg gag aaa gcc tcg tta aaa tgt gcc cag tat tgg cca cag aaa
363 Ile Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys 503
364 115 120 125
366 gaa gaa aaa gag atg gtc ttc gat gac acc aat ttg aag ctg aca ctg
367 Glu Glu Lys Glu Met Val Phe Asp Asp Thr Asn Leu Lys Leu Thr Leu 551
368 130 135 140
370 atc tot gaa gat gtc aag tca tat tac aca gta cgg cag ttg gag ttg
371 Ile Ser Glu Asp Val Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu 599
372 145 150 155 160

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

6/5/01

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/854,883

DATE: 06/05/2001

TIME: 08:27:25

Input Set : A:\es.txt

Output Set: C:\CRF3\06052001\I854883.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:567 M:283 W: Missing Blank Line separator, <220> field identifier
L:639 M:283 W: Missing Blank Line separator, <400> field identifier
L:3886 M:283 W: Missing Blank Line separator, <220> field identifier
L:3890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242